

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 09/117,246C
Source: IFW16
Date Processed by STIC: 3/8/06

ENTERED



IFW16

RAW SEQUENCE LISTING DATE: 03/08/2006
 PATENT APPLICATION: US/09/117,246C TIME: 11:53:26

Input Set : A:\.txt
 Output Set: N:\CRF4\03072006\I117246C.raw

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3 <110> APPLICANT: Ludevid, Dolores
4      Torrent, Margarita
5      Alvarez, Inaki
6      Perez, Pascual
8 <120> TITLE OF INVENTION: Amino acid-enriched plant protein reserves, particularly
9      lysine-enriched maize-zein, and plants expressing such proteins
11 <130> FILE REFERENCE: 50062/004001
13 <140> CURRENT APPLICATION NUMBER: US 09/117,246C
14 <141> CURRENT FILING DATE: 1998-12-03
16 <150> PRIOR APPLICATION NUMBER: PCT/FR97/00167
17 <151> PRIOR FILING DATE: 1997-01-28
19 <150> PRIOR APPLICATION NUMBER: FR96/01004
20 <151> PRIOR FILING DATE: 1996-01-29
22 <160> NUMBER OF SEQ ID NOS: 24
24 <170> SOFTWARE: PatentIn version 3.3
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 44
28 <212> TYPE: DNA
29 <213> ORGANISM: Artificial Sequence
31 <220> FEATURE:
32 <223> OTHER INFORMATION: based on Maize
34 <400> SEQUENCE: 1
35 cgatgaattc aaaccaaagc caaagccgaa gccaaaagaa ttca                      44
38 <210> SEQ ID NO: 2
39 <211> LENGTH: 46
40 <212> TYPE: DNA
41 <213> ORGANISM: Artificial Sequence
43 <220> FEATURE:
44 <223> OTHER INFORMATION: based on Maize
46 <400> SEQUENCE: 2
47 agcttgaatt cttttggcctt cggctttggc tttggtttga attcat                  46
50 <210> SEQ ID NO: 3
51 <211> LENGTH: 17
52 <212> TYPE: PRT
53 <213> ORGANISM: Maize
55 <400> SEQUENCE: 3
57 Ile Glu Phe Lys Pro Lys Pro Lys Pro Lys Pro Lys Glu Phe Leu Gln
58 1           5           10           15
61 Pro
65 <210> SEQ ID NO: 4
66 <211> LENGTH: 28
67 <212> TYPE: PRT
68 <213> ORGANISM: Maize

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70 <400> SEQUENCE: 4
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73 1 5 10 15
76 Lys Pro Lys Pro Lys Pro Lys Glu Phe Leu Gln Pro
77 20 25
80 <210> SEQ ID NO: 5
81 <211> LENGTH: 20
82 <212> TYPE: PRT
83 <213> ORGANISM: Maize
85 <400> SEQUENCE: 5
87 Asp Gly Ile Asp Glu Phe Lys Pro Lys Pro Lys Pro Lys Pro Lys Glu
88 1 5 10 15
91 Phe Lys Leu Asp
92 20
95 <210> SEQ ID NO: 6
96 <211> LENGTH: 672
97 <212> TYPE: DNA
98 <213> ORGANISM: Maize
101 <220> FEATURE:
102 <221> NAME/KEY: CDS
103 <222> LOCATION: (1)..(672)
105 <400> SEQUENCE: 6
106 atg agg gtg ttg ctc gtt gcc ctc gct ctc ctg gct ctc gct gcg agc 48
107 Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
108 1 5 10 15
110 gcc acc tcc acg cat aca agc ggc ggc tgc ggc tgc cag cca ccg ccg 96
111 Ala Thr Ser Thr His Thr Ser Gly Gly Cys Gly Cys Gln Pro Pro Pro
112 20 25 30
114 ccg gtt cat cta ccg ccg ccg gtg cat ctg cca cct ccg gtt cac ctg 144
115 Pro Val His Leu Pro Pro Pro Val His Leu Pro Pro Pro Val His Leu
116 35 40 45
118 cca cct ccg gtg cat ctc cca ccg ccg gtc cac ctg ccg ccg ccg gtc 192
119 Pro Pro Pro Val His Leu Pro Pro Pro Val His Leu Pro Pro Pro Val
120 50 55 60
122 cac ctg cca ccg ccg gtc cat gtg ccg ccg ccg gtt cat ctg ccg ccg 240
123 His Leu Pro Pro Pro Val His Val Pro Pro Pro Val His Leu Pro Pro
124 65 70 75 80
126 cca cca tgc cac tac cct act caa ccg ccc ccg cct cag cct cat ccc 288
127 Pro Pro Cys His Tyr Pro Thr Gln Pro Pro Arg Pro Gln Pro His Pro
128 85 90 95
130 cag cca cac cca tgc ccg tgc caa cag ccg cat cca agc ccg tgc cag 336
131 Gln Pro His Pro Cys Pro Cys Gln Gln Pro His Pro Ser Pro Cys Gln
132 100 105 110
134 ctg cag gga acc tgc ggc gtt ggc agc acc ccg atc ctg ggc cag tgc 384
135 Leu Gln Gly Thr Cys Gly Val Gly Ser Thr Pro Ile Leu Gly Gln Cys
136 115 120 125
138 gtc gag ttt ctg agg cat cag tgc agc ccg acg gcg acg ccc tac tgc 432
139 Val Glu Phe Leu Arg His Gln Cys Ser Pro Thr Ala Thr Pro Tyr Cys
140 130 135 140

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142 tcg cct cag tgc cag tcg ttg cgg cag cag tgt tgc cag cag ctc agg      480
143 Ser Pro Gln Cys Gln Ser Leu Arg Gln Gln Cys Cys Gln Gln Leu Arg
144 145                               150                               155                               160
146 cag gtg gag ccg cag cac cgg tac cag gcg atc ttc ggc ttg gtc ctc      528
147 Gln Val Glu Pro Gln His Arg Tyr Gln Ala Ile Phe Gly Leu Val Leu
148                               165                               170                               175
150 cag tcc atc ctg cag cag cag ccg caa agc ggc cag gtc gcg ggg ctg      576
151 Gln Ser Ile Leu Gln Gln Gln Pro Gln Ser Gly Gln Val Ala Gly Leu
152                               180                               185                               190
154 ttg gcg gcg cag ata gcg cag caa ctg acg gcg atg tgc ggc ctg cag      624
155 Leu Ala Ala Gln Ile Ala Gln Gln Leu Thr Ala Met Cys Gly Leu Gln
156                               195                               200                               205
158 cag ccg act cca tgc ccc tac gct gct gcc ggc ggt gtc ccc cac tga      672
159 Gln Pro Thr Pro Cys Pro Tyr Ala Ala Ala Gly Gly Val Pro His
160 210                               215                               220
163 <210> SEQ ID NO: 7
164 <211> LENGTH: 223
165 <212> TYPE: PRT
166 <213> ORGANISM: Maize
168 <400> SEQUENCE: 7
170 Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
171 1                               5                               10                               15
174 Ala Thr Ser Thr His Thr Ser Gly Gly Cys Gly Cys Gln Pro Pro Pro
175 20                               25                               30
178 Pro Val His Leu Pro Pro Pro Val His Leu Pro Pro Pro Val His Leu
179 35                               40                               45
182 Pro Pro Pro Val His Leu Pro Pro Pro Val His Leu Pro Pro Pro Val
183 50                               55                               60
186 His Leu Pro Pro Pro Val His Val Pro Pro Pro Val His Leu Pro Pro
187 65                               70                               75                               80
190 Pro Pro Cys His Tyr Pro Thr Gln Pro Pro Arg Pro Gln Pro His Pro
191 85                               90                               95
194 Gln Pro His Pro Cys Pro Cys Gln Gln Pro His Pro Ser Pro Cys Gln
195 100                              105                              110
198 Leu Gln Gly Thr Cys Gly Val Gly Ser Thr Pro Ile Leu Gly Gln Cys
199 115                              120                              125
202 Val Glu Phe Leu Arg His Gln Cys Ser Pro Thr Ala Thr Pro Tyr Cys
203 130                              135                              140
206 Ser Pro Gln Cys Gln Ser Leu Arg Gln Gln Cys Cys Gln Gln Leu Arg
207 145                              150                              155                              160
210 Gln Val Glu Pro Gln His Arg Tyr Gln Ala Ile Phe Gly Leu Val Leu
211 165                              170                              175
214 Gln Ser Ile Leu Gln Gln Gln Pro Gln Ser Gly Gln Val Ala Gly Leu
215 180                              185                              190
218 Leu Ala Ala Gln Ile Ala Gln Gln Leu Thr Ala Met Cys Gly Leu Gln
219 195                              200                              205
222 Gln Pro Thr Pro Cys Pro Tyr Ala Ala Ala Gly Gly Val Pro His
223 210                              215                              220
226 <210> SEQ ID NO: 8

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227 <211> LENGTH: 693
228 <212> TYPE: DNA
229 <213> ORGANISM: maize
232 <220> FEATURE:
233 <221> NAME/KEY: CDS
234 <222> LOCATION: (1)..(693)
236 <400> SEQUENCE: 8
237 atg agg gtg ttg ctc gtt gcc ctc gct ctc ctg gct ctc gct gcg agc      48
238 Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
239 1 5 10 15
241 gcc acc tcc acg cat aca agc ggc ggc tgc ggc tgc cag cca ccg ccg      96
242 Ala Thr Ser Thr His Thr Ser Gly Gly Cys Gly Cys Gln Pro Pro Pro
243 20 25 30
245 ccg gtt cat cta ccg ccg ccg gtg cat ctg cca cct ccg gtt cac ctg      144
246 Pro Val His Leu Pro Pro Pro Val His Leu Pro Pro Pro Val His Leu
247 35 40 45
249 cca cct ccg gtg cat ctc cca ccg ccg gtc cac ctg ccg ccg ccg gtc      192
250 Pro Pro Pro Val His Leu Pro Pro Pro Val His Leu Pro Pro Pro Val
251 50 55 60
253 cac ctg cca ccg ccg gtc cat gtg ccg ccg ccg gtt cat ctg ccg ccg      240
254 His Leu Pro Pro Pro Val His Val Pro Pro Pro Val His Leu Pro Pro
255 65 70 75 80
257 cca cca tgc cac tac cct act caa ccg ccc cgg atc gaa ttc aaa cca      288
258 Pro Pro Cys His Tyr Pro Thr Gln Pro Pro Arg Ile Glu Phe Lys Pro
259 85 90 95
261 aag cca aag ccg aag cca aaa gaa ttc aaa cca aag cca aag ccg aag      336
262 Lys Pro Lys Pro Lys Pro Lys Glu Phe Lys Pro Lys Pro Lys Pro Lys
263 100 105 110
265 cca aaa gaa ttc ctg cag ccc ctg cag gga acc tgc ggc gtt ggc agc      384
266 Pro Lys Glu Phe Leu Gln Pro Leu Gln Gly Thr Cys Gly Val Gly Ser
267 115 120 125
269 acc ccg atc ctg ggc cag tgc gtc gag ttt ctg agg cat cag tgc agc      432
270 Thr Pro Ile Leu Gly Gln Cys Val Glu Phe Leu Arg His Gln Cys Ser
271 130 135 140
273 ccg acg gcg acg ccc tac tgc tcg cct cag tgc cag tcg ttg cgg cag      480
274 Pro Thr Ala Thr Pro Tyr Cys Ser Pro Gln Cys Gln Ser Leu Arg Gln
275 145 150 155 160
277 cag tgt tgc cag cag ctc agg cag gtg gag ccg cag cac cgg tac cag      528
278 Gln Cys Cys Gln Gln Leu Arg Gln Val Glu Pro Gln His Arg Tyr Gln
279 165 170 175
281 gcg atc ttc ggc ttg gtc ctc cag tcc atc ctg cag cag cag ccg caa      576
282 Ala Ile Phe Gly Leu Val Leu Gln Ser Ile Leu Gln Gln Gln Pro Gln
283 180 185 190
285 agc ggc cag gtc gcg ggg ctg ttg gcg gcg cag ata gcg cag caa ctg      624
286 Ser Gly Gln Val Ala Gly Leu Leu Ala Ala Gln Ile Ala Gln Gln Leu
287 195 200 205
289 acg gcg atg tgc ggc ctg cag cag ccg act cca tgc ccc tac gct gct      672
290 Thr Ala Met Cys Gly Leu Gln Gln Pro Thr Pro Cys Pro Tyr Ala Ala
291 210 215 220

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293 gcc ggc ggt gtc ccc cac tga
294 Ala Gly Gly Val Pro His
295 225 230
298 <210> SEQ ID NO: 9
299 <211> LENGTH: 230
300 <212> TYPE: PRT
301 <213> ORGANISM: maize
303 <400> SEQUENCE: 9
305 Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
306 1 5 10 15
309 Ala Thr Ser Thr His Thr Ser Gly Gly Cys Gly Cys Gln Pro Pro Pro
310 20 25 30
313 Pro Val His Leu Pro Pro Pro Val His Leu Pro Pro Pro Val His Leu
314 35 40 45
317 Pro Pro Pro Val His Leu Pro Pro Pro Val His Leu Pro Pro Pro Val
318 50 55 60
321 His Leu Pro Pro Pro Val His Val Pro Pro Pro Val His Leu Pro Pro
322 65 70 75 80
325 Pro Pro Cys His Tyr Pro Thr Gln Pro Pro Arg Ile Glu Phe Lys Pro
326 85 90 95
329 Lys Pro Lys Pro Lys Pro Lys Glu Phe Lys Pro Lys Pro Lys Pro Lys
330 100 105 110
333 Pro Lys Glu Phe Leu Gln Pro Leu Gln Gly Thr Cys Gly Val Gly Ser
334 115 120 125
337 Thr Pro Ile Leu Gly Gln Cys Val Glu Phe Leu Arg His Gln Cys Ser
338 130 135 140
341 Pro Thr Ala Thr Pro Tyr Cys Ser Pro Gln Cys Gln Ser Leu Arg Gln
342 145 150 155 160
345 Gln Cys Cys Gln Gln Leu Arg Gln Val Glu Pro Gln His Arg Tyr Gln
346 165 170 175
349 Ala Ile Phe Gly Leu Val Leu Gln Ser Ile Leu Gln Gln Gln Pro Gln
350 180 185 190
353 Ser Gly Gln Val Ala Gly Leu Leu Ala Ala Gln Ile Ala Gln Gln Leu
354 195 200 205
357 Thr Ala Met Cys Gly Leu Gln Gln Pro Thr Pro Cys Pro Tyr Ala Ala
358 210 215 220
361 Ala Gly Gly Val Pro His
362 225 230
365 <210> SEQ ID NO: 10
366 <211> LENGTH: 723
367 <212> TYPE: DNA
368 <213> ORGANISM: Maize
371 <220> FEATURE:
372 <221> NAME/KEY: CDS
373 <222> LOCATION: (1)..(723)
375 <400> SEQUENCE: 10
376 atg agg gtg ttg ctc gtt gcc ctc gct ctc ctg gct ctc gct gcg agc
377 Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
378 1 5 10 15

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48

RAW SEQUENCE LISTING ERROR SUMMARY
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Base Note:

One or more of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> <223> fields of each sequence which presents at least one n or Xaa.

Seq#:22; Xaa Pos. 5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25
Seq#:22; Xaa Pos. 26,27,28,29,30,31,32,33,34,35,36,37,38,39,40,41,42,43,44
Seq#:22; Xaa Pos. 45,46,47,48,49,50,51,52,53,54,55,56,57,58,59,60

VERIFICATION SUMMARY

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349 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22 after pos.:0
341 Repeated in SeqNo=22